

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/574,045  
Source: TFWP  
Date Processed by STIC: 04/07/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 04/07/2006

PATENT APPLICATION: US/10/574,045

TIME: 11:02:40

Input Set : A:\14875-157US1.txt

Output Set: N:\CRF4\04072006\J574045.raw

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3 <110> APPLICANT: Matsushima, Kouji
4      Hashimoto, Shinichi
5      Tsuchiya, Masayuki
6      Hirata, Yuichi
7      Yoshida, Kenji
8      Ojima, Kazuyuki
10 <120> TITLE OF INVENTION: PROTEIN EXPRESSED IN NK CELL
12 <130> FILE REFERENCE: 14875-157US1
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/574,045
C--> 14 <141> CURRENT FILING DATE: 2005-03-28
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/14207
15 <151> PRIOR FILING DATE: 2004-09-29
17 <150> PRIOR APPLICATION NUMBER: JP 2003-338331
18 <151> PRIOR FILING DATE: 2003-09-29
20 <160> NUMBER OF SEQ ID NOS: 53
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1473
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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30 <221> NAME/KEY: CDS
31 <222> LOCATION: (87)..(1376)
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38                               Met Leu Pro Ser Leu Val Pro Cys Val
39                               1           5
41 ggg aaa act gtc tgg ctg tac ctc caa gcc tgg cca aac cct gtg ttt 161
42 Gly Lys Thr Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe
43 10                15                20                25
45 gaa gga gat gcc ctg act ctg cga tgt cag gga tgg aag aat aca cca 209
46 Glu Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro
47                30                35                40
49 ctg tct cag gtg aag ttc tac aga gat gga aaa ttc ctt cat ttc tct 257
50 Leu Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser
51                45                50                55
53 aag gaa aac cag act ctg tcc atg gga gca gca aca gtg cag agc cgt 305
54 Lys Glu Asn Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg
55                60                65                70
57 ggc cag tac agc tgc tct ggg cag gtg atg tat att cca cag aca ttc 353
58 Gly Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe
59    75                80                85

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61	aca	caa	act	tca	gag	act	gcc	atg	gtt	caa	gtc	caa	gag	ctg	ttt	cca	401
62	Thr	Gln	Thr	Ser	Glu	Thr	Ala	Met	Val	Gln	Val	Gln	Glu	Leu	Phe	Pro	
63	90					95					100					105	
65	cct	cct	gtg	ctg	agt	gcc	atc	ccc	tct	cct	gag	ccc	cga	gag	ggg	agc	449
66	Pro	Pro	Val	Leu	Ser	Ala	Ile	Pro	Ser	Pro	Glu	Pro	Arg	Glu	Gly	Ser	
67					110					115					120		
69	ctg	gtg	acc	ctg	aga	tgt	cag	aca	aag	ctg	cac	ccc	ctg	agg	tca	gcc	497
70	Leu	Val	Thr	Leu	Arg	Cys	Gln	Thr	Lys	Leu	His	Pro	Leu	Arg	Ser	Ala	
71				125					130				135				
73	ttg	agg	ctc	ctt	ttc	tcc	ttc	cac	aag	gac	ggc	cac	acc	ttg	cag	gac	545
74	Leu	Arg	Leu	Leu	Phe	Ser	Phe	His	Lys	Asp	Gly	His	Thr	Leu	Gln	Asp	
75		140					145						150				
77	agg	ggc	cct	cac	cca	gaa	ctc	tgc	atc	ccg	gga	gcc	aag	gag	gga	gac	593
78	Arg	Gly	Pro	His	Pro	Glu	Leu	Cys	Ile	Pro	Gly	Ala	Lys	Glu	Gly	Asp	
79		155				160					165						
81	tct	ggg	ctt	tac	tgg	tgt	gag	gtg	gcc	cct	gag	ggg	ggc	cag	gtc	cag	641
82	Ser	Gly	Leu	Tyr	Trp	Cys	Glu	Val	Ala	Pro	Glu	Gly	Gly	Gln	Val	Gln	
83	170					175					180					185	
85	aag	cag	agg	ccc	cag	ctg	gag	gtc	aga	gtg	cag	gct	cct	gta	tcc	cgt	689
86	Lys	Gln	Ser	Pro	Gln	Leu	Glu	Val	Arg	Val	Gln	Ala	Pro	Val	Ser	Arg	
87				190					195					200			
89	cct	gtg	ctc	act	ctg	cac	cac	ggg	cct	gct	gac	cct	gct	gtg	ggg	gac	737
90	Pro	Val	Leu	Thr	Leu	His	His	Gly	Pro	Ala	Asp	Pro	Ala	Val	Gly	Asp	
91				205					210					215			
93	atg	gtg	cag	ctc	ctc	tgt	gag	gca	cag	agg	ggc	tcc	cct	ccg	atc	ctg	785
94	Met	Val	Gln	Leu	Leu	Cys	Glu	Ala	Gln	Arg	Gly	Ser	Pro	Pro	Ile	Leu	
95		220						225					230				
97	tat	tcc	ttc	tac	ctt	gat	gag	aag	att	gtg	ggg	aac	cac	tca	gct	ccc	833
98	Tyr	Ser	Phe	Tyr	Leu	Asp	Glu	Lys	Ile	Val	Gly	Asn	His	Ser	Ala	Pro	
99		235				240					245						
101	tgt	ggg	gga	acc	acc	tcc	ctc	ctc	ttc	cca	gtg	aag	tca	gaa	cag	gat	881
102	Cys	Gly	Gly	Thr	Thr	Ser	Leu	Leu	Phe	Pro	Val	Lys	Ser	Glu	Gln	Asp	
103	250					255					260					265	
105	gct	ggg	aac	tac	tcc	tgc	gag	gct	gag	aac	agt	gtc	tcc	aga	gag	agg	929
106	Ala	Gly	Asn	Tyr	Ser	Cys	Glu	Ala	Glu	Asn	Ser	Val	Ser	Arg	Glu	Arg	
107				270					275					280			
109	agt	gag	ccc	aag	aag	ctg	tct	ctg	aag	ggg	tct	caa	gtc	ttg	ttc	act	977
110	Ser	Glu	Pro	Lys	Lys	Leu	Ser	Leu	Lys	Gly	Ser	Gln	Val	Leu	Phe	Thr	
111				285					290					295			
113	ccc	gcc	agc	aac	tgg	ctg	gtt	cct	tgg	ctt	cct	gcg	agc	ctg	ctt	ggc	1025
114	Pro	Ala	Ser	Asn	Trp	Leu	Val	Pro	Trp	Leu	Pro	Ala	Ser	Leu	Leu	Gly	
115		300						305					310				
117	ctg	atg	gtt	att	gct	gct	gca	ctt	ctg	gtt	tat	gtg	aga	tcc	tgg	aga	1073
118	Leu	Met	Val	Ile	Ala	Ala	Ala	Leu	Leu	Val	Tyr	Val	Arg	Ser	Trp	Arg	
119		315					320						325				
121	aaa	gct	ggg	ccc	ctt	cca	tcc	cag	ata	cca	ccc	aca	gct	cca	ggg	gga	1121
122	Lys	Ala	Gly	Pro	Leu	Pro	Ser	Gln	Ile	Pro	Pro	Thr	Ala	Pro	Gly	Gly	
123	330					335					340				345		
125	gag	cag	tgc	cca	cta	tat	gcc	aac	gtg	cat	cac	cag	aaa	ggg	aaa	gat	1169

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126 Glu Gln Cys Pro Leu Tyr Ala Asn Val His His Gln Lys Gly Lys Asp
127          350          355          360
129 gaa ggt gtt gtc tac tct gtg gtg cat aga acc tca aag agg agt gaa 1217
130 Glu Gly Val Val Tyr Ser Val Val His Arg Thr Ser Lys Arg Ser Glu
131          365          370          375
133 gcc agg tct gct gag ttc acc gtg ggg aga aag gac agt tct atc atc 1265
134 Ala Arg Ser Ala Glu Phe Thr Val Gly Arg Lys Asp Ser Ser Ile Ile
135          380          385          390
137 tgt gcg gag gtg aga tgc ctg cag ccc agt gag gtt tca tcc acg gag 1313
138 Cys Ala Glu Val Arg Cys Leu Gln Pro Ser Glu Val Ser Ser Thr Glu
139          395          400          405
141 gtg aat atg aga agc agg act ctc caa gaa ccc ctt agc gac tgt gag 1361
142 Val Asn Met Arg Ser Arg Thr Leu Gln Glu Pro Leu Ser Asp Cys Glu
143 410          415          420          425
145 gag gtt ctc tgc tag tgatggtgtt ctccatcaaa cacacgcccc cccccagtct 1416
146 Glu Val Leu Cys
149 ccagtgtctcc tcaggaagac agtgggggtcc tcaactcttt ctgtgggtcc ttcagtg 1473
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153 <211> LENGTH: 429
154 <212> TYPE: PRT
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157 <400> SEQUENCE: 2
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159 1          5          10          15
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162          20          25          30
164 Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln Val Lys Phe Tyr
165          35          40          45
167 Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn Gln Thr Leu Ser
168          50          55          60
170 Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly
171 65          70          75          80
173 Gln Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala
174          85          90          95
176 Met Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile
177          100          105          110
179 Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln
180          115          120          125
183 Thr Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe
184          130          135          140
186 His Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu
187 145          150          155          160
189 Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu
190          165          170          175
192 Val Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser Pro Gln Leu Glu
193          180          185          190
195 Val Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His
196          195          200          205
198 Gly Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu

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199      210      215      220
201 Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu
202 225      230      235      240
204 Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu
205      245      250      255
207 Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu
208      260      265      270
210 Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser
211      275      280      285
213 Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val
214      290      295      300
216 Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala
217 305      310      315      320
219 Leu Leu Val Tyr Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser
220      325      330      335
222 Gln Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala
223      340      345      350
225 Asn Val His His Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val
226      355      360      365
228 Val His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr
229      370      375      380
231 Val Gly Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu
232 385      390      395      400
234 Gln Pro Ser Glu Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr
235      405      410      415
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238      420      425
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244 <213> ORGANISM: Homo sapiens
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247 <221> NAME/KEY: CDS
248 <222> LOCATION: (88)..(1410)
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254 aagagaacga tagaggaaaa tatatga atg ttg cca tct tta ggc ccc atg ctg      114
255      Met Leu Pro Ser Leu Gly Pro Met Leu
256      1      5
258 ctc tgg acg gct gtg ctg ctc ttt gtt ccc tgt gtt ggg aaa act gtc      162
259 Leu Trp Thr Ala Val Leu Leu Phe Val Pro Cys Val Gly Lys Thr Val
260 10      15      20      25
262 tgg ctg tac ctc caa gcc tgg cca aac cct gtg ttt gaa gga gat gcc      210
263 Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu Gly Asp Ala
264      30      35      40
266 ctg act ctg cga tgt cag gga tgg aag aat aca cca ctg tct cag gtg      258
267 Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln Val
268      45      50      55
270 aag ttc tac aga gat gga aaa ttc ctt cat ttc tct aag gaa aac cag      306

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271	Lys	Phe	Tyr	Arg	Asp	Gly	Lys	Phe	Leu	His	Phe	Ser	Lys	Glu	Asn	Gln	
272			60					65					70				
274	act	ctg	tcc	atg	gga	gca	gca	aca	gtg	cag	agc	cgt	ggc	cag	tac	agc	354
275	Thr	Leu	Ser	Met	Gly	Ala	Ala	Thr	Val	Gln	Ser	Arg	Gly	Gln	Tyr	Ser	
276		75						80				85					
278	tgc	tct	ggg	cag	gtg	atg	tat	att	cca	cag	aca	ttc	aca	caa	act	tca	402
279	Cys	Ser	Gly	Gln	Val	Met	Tyr	Ile	Pro	Gln	Thr	Phe	Thr	Gln	Thr	Ser	
280	90					95					100					105	
282	gag	act	gcc	atg	gtt	caa	gtc	caa	gag	ctg	ttt	cca	cct	cct	gtg	ctg	450
283	Glu	Thr	Ala	Met	Val	Gln	Val	Gln	Glu	Leu	Phe	Pro	Pro	Pro	Val	Leu	
284					110					115					120		
286	agt	gcc	atc	ccc	tct	cct	gag	ccc	cga	gag	ggg	agc	ctg	gtg	acc	ctg	498
287	Ser	Ala	Ile	Pro	Ser	Pro	Glu	Pro	Arg	Glu	Gly	Ser	Leu	Val	Thr	Leu	
288				125					130					135			
290	aga	tgt	cag	aca	aag	ctg	cac	ccc	ctg	agg	tca	gcc	ttg	agg	ctc	ctt	546
291	Arg	Cys	Gln	Thr	Lys	Leu	His	Pro	Leu	Arg	Ser	Ala	Leu	Arg	Leu	Leu	
292			140					145				150					
294	ttc	tcc	ttc	cac	aag	gac	ggc	cac	acc	ttg	cag	gac	agg	ggc	cct	cac	594
295	Phe	Ser	Phe	His	Lys	Asp	Gly	His	Thr	Leu	Gln	Asp	Arg	Gly	Pro	His	
296		155					160					165					
298	cca	gaa	ctc	tgc	atc	ccg	gga	gcc	aag	gag	gga	gac	tct	ggg	ctt	tac	642
299	Pro	Glu	Leu	Cys	Ile	Pro	Gly	Ala	Lys	Glu	Gly	Asp	Ser	Gly	Leu	Tyr	
300	170					175					180				185		
302	tgg	tgt	gag	gtg	gcc	cct	gag	ggg	ggc	cag	gtc	cag	aag	cag	agc	ccc	690
303	Trp	Cys	Glu	Val	Ala	Pro	Glu	Gly	Gly	Gln	Val	Gln	Lys	Gln	Ser	Pro	
304				190						195					200		
306	cag	ctg	gag	gtc	aga	gtg	cag	gct	cct	gta	tcc	cgt	cct	gtg	ctc	act	738
307	Gln	Leu	Glu	Val	Arg	Val	Gln	Ala	Pro	Val	Ser	Arg	Pro	Val	Leu	Thr	
308				205						210				215			
310	ctg	cac	cac	ggg	cct	gct	gac	ccc	gct	gtg	ggg	gac	atg	gtg	cag	ctc	786
311	Leu	His	His	Gly	Pro	Ala	Asp	Pro	Ala	Val	Gly	Asp	Met	Val	Gln	Leu	
312			220					225				230					
314	ctc	tgt	gag	gca	cag	agg	ggc	tcc	cct	ccg	atc	ctg	tat	tcc	ttc	tac	834
315	Leu	Cys	Glu	Ala	Gln	Arg	Gly	Ser	Pro	Pro	Ile	Leu	Tyr	Ser	Phe	Tyr	
316		235					240					245					
318	ctt	gat	gag	aag	att	gtg	ggg	aac	cac	tca	gct	ccc	tgt	ggg	gga	acc	882
319	Leu	Asp	Glu	Lys	Ile	Val	Gly	Asn	His	Ser	Ala	Pro	Cys	Gly	Gly	Thr	
320	250					255					260				265		
322	acc	tcc	ctc	ctc	ttc	cca	gtg	aag	tca	gaa	cag	gat	gct	ggg	aac	tac	930
323	Thr	Ser	Leu	Leu	Phe	Pro	Val	Lys	Ser	Glu	Gln	Asp	Ala	Gly	Asn	Tyr	
324				270						275					280		
326	tcc	tgc	gag	gct	gag	aac	agt	gtc	tcc	aga	gag	agg	agt	gag	ccc	aag	978
327	Ser	Cys	Glu	Ala	Glu	Asn	Ser	Val	Ser	Arg	Glu	Arg	Ser	Glu	Pro	Lys	
328				285						290				295			
330	aag	ctg	tct	ctg	aag	ggg	tct	caa	gtc	ttg	ttc	act	ccc	gcc	agc	aac	1026
331	Lys	Leu	Ser	Leu	Lys	Gly	Ser	Gln	Val	Leu	Phe	Thr	Pro	Ala	Ser	Asn	
332			300					305				310					
334	tgg	ctg	gtt	cct	tgg	ctt	cct	gcg	agc	ctg	ctt	ggc	ctg	atg	gtt	att	1074
335	Trp	Leu	Val	Pro	Trp	Leu	Pro	Ala	Ser	Leu	Leu	Gly	Leu	Met	Val	Ile	

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31

Seq#: 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53

**VERIFICATION SUMMARY**

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date